

10/551878

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K3176SEQ.TXT

SEQUENCE LISTING

<110> Deutsches Krebsforschungszentrum Stiftung des öffentlichen
Rechts
Ponstingl, Herwig
Zimmermann, Hans-Peter
Marmé, Alexander
Bastert, Gunther
Kurek, Raffael
Wallwiener, Diethelm

<120> Drop1, a novel marker for carcinomas

<130> K 3176

<140> PCT/EP2004/003538
<141> 2004-04-02

<150> EP 03007680.6
<151> 2003-04-03

<160> 30

<170> PatentIn version 3.2

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| aacagaacac | aactgccagt | gggtgtgagc | tcatgcacac | ggagatgcag | gccctgcgtg | 9240 |
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<210> 10
 <211> 1746
 <212> DNA
 <213> homo sapiens

| | |
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| | 60 |
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| cttaaaacgg | aagaagaaaa |
| agaagcagtt | cagtcttttg |
| | 120 |
| gagagctgcc | tccttggtga |
| gtgctgcaaa | ggcctggaat |
| tcatttatga | cagaatagat |
| | 180 |
| ctagaaaagt | ccaagcatgt |
| tttctagagt | ggtgtagccc |
| tgtgctgcct | ccagtgaaga |
| | 240 |
| gtctcttggt | gttggcttcg |
| tgcttccgga | gggacctagg |
| caacctccag | aggggcctcc |
| | 300 |
| cggtgtcctc | gggatatcgc |
| caatgtgatg | cagaggctgc |
| aagatgagca | agagatagta |
| | 360 |
| caaaaacgaa | ctttcacaaa |
| atggatcaac | tctcatctgg |
| ccaagcggaa | acctccaatg |
| | 420 |
| gtgggtggacg | atctttttga |
| agacatgaaa | gatgggtgta |
| aactgcttgc | ccttctggag |
| | 480 |
| gtcctgtctg | ggcagaaact |
| gccttgtaga | caaggacgcc |
| ggatgaagcg | aatccatgct |
| | 540 |
| gtggctaaca | ttggcacggc |
| actcaagttc | ctcgaaggaa |
| gaaagattaa | attagtcaac |
| | 600 |
| attaactcca | ccgatatagc |
| tgatggccga | ccctcaatag |
| ttcttggatt | gatgtggacc |
| | 660 |
| attattctat | atttccagat |
| tgaagagttg | accagcaacc |
| tgccccagct | ccagtctttg |
| | 720 |
| tccagcagcg | catcctccgt |
| ggacagcata | gttagctctg |
| agactcccag | cccaccaagt |
| | 780 |
| aaacggaagg | tgaccaccaa |
| gatccaagga | aatactaaga |
| aggctttatt | aaagtgggtt |
| | 840 |
| cagtacacag | ctggcaagca |
| gactggaata | gaagtaaaaag |
| attttgggaa | gagttggaga |
| | 900 |
| agcgggggtg | cctttcattc |
| agttattcat | gccattcgac |
| cggaattggg | ggacttggag |
| | 960 |
| acagtgaaag | gcagatccaa |
| ccgagaaaat | ttggagggatg |
| ctttcactat | cgccgaaaca |
| | 1020 |
| gaactgggga | tccaagact |
| gctagatcct | gaagacgttg |
| atgtggataa | accagatgag |
| | 1080 |

K3176SEQ.TXT

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<213> Homo sapiens

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agaagtaaaa gatthttggga agagtggag aagcgggggt gcctttcatt cagttattca 660
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K3176SEQ.TXT

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| tgaagacgtt gatgtggata aaccagatga gaaatctatt atgacctatg tagcccagtt | 840 |
| tctgaaacat taccctgaca tccacaatgc aagcactgat gggcaagagg atgatagaga | 900 |
| agacagagta atttttaagg aaatgaaagt ttggatagaa caatttgaga gagatttgac | 960 |
| aagagcacag atggtggaat caaatttaca ggataaatat cagtcattta agcacttcag | 1020 |
| agttcaatat gaaatgaaga ggaaacagat tgaacattta atacaacat tacacagaga | 1080 |
| cggtaaattg tcacttgacc aagcattggt aaaacaatct tgggatagag tgacctccag | 1140 |
| gctctttgac tggcatatac agcttgataa atctcttcct gcacctctgg gcaccagggc | 1200 |
| cc | 1202 |

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| <400> 13 | |
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<210> 14
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| | |
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| <400> 14 | |
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| | |
|--|-----|
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| atttaagcac ttcagagttc aatatgaaat gaagaggaaa cagattgaac atttaatata | 120 |
| accattacac agagacggta aattgtcact tgaccaagca ttggtaaaac aatcttgagg | 180 |
| tagagtgacc tccaggctct ttgactggca tatacagctt gataaatctc ttcctgcacc | 240 |
| tctgggcacc ataggtgcct ggctgtacag agcggagggtg gccctgagag aggaaataac | 300 |
| cgttcaacag gtccacgagg aaacagcaaa cacgatacaa cggaaacttg agcaacataa | 360 |
| ggatctgctt caaaacacgg atgcccacaa aagagcattc catgaaatct accggaccag | 420 |
| gtctgttaac gggattccag tgccacctga tcaattagag gacatggccg agaggtttca | 480 |
| ttttgtttcc tccacatcag agctacacct aatgaaaatg gaatttttag aattaaagta | 540 |
| ccgtctgctc tcaactgctg ttcttgacga gtcaaagctg aagtcttgga tcattaagta | 600 |

K3176SEQ.TXT

| | | | | | | |
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| cgggaggaga | gagtcagtgg | agcagcttct | acaaaactac | gtgtctttta | tagaaaatag | 660 |
| caagttcttt | gaacaatatg | aggtagacata | ccagatcttg | aaacagacag | ctgagatgta | 720 |
| tgtcaaagca | gatggttcag | tggaagaagc | tgagaatgtg | atgaaattca | tgaatgaaac | 780 |
| caccgctcag | tggaggaatc | tctcagtaga | agtgaggagt | gtgaggagca | tgctggaaga | 840 |
| agtgatctct | aactgggatc | gctatggcaa | tacagtggct | agtctgcaag | cctggctaga | 900 |
| ggatgctgaa | aaaatgctca | atcaatcaga | aaatgccaaa | aaggattttt | ttcgaaattt | 960 |
| acctcattgg | attcagcagc | atactgccat | gaacgatgct | ggcaattttc | taattgaaac | 1020 |
| ctgtgatgag | atggtttccc | gtgacctgaa | gcagcaatta | ctgttgctaa | atgggcggtg | 1080 |
| gagggagtgt | tttatggaag | tcaagcaata | tgctcaagct | gatgagatgg | acagaatgaa | 1140 |
| gaaggaatac | acagactgtg | ttgttaccct | gtctgctttt | gcaacggaag | cccataagaa | 1200 |
| actttctgaa | cccttagaag | tctcttttat | gaatgtcaag | ctattaattc | aagacttgga | 1260 |
| ggatattgag | cagaggggtg | ctgtgatgga | tgccaatac | aagataatta | caaagacagc | 1320 |
| acacctcatt | gccaaagaaa | gcccccaaga | agaaggaaaa | gaaatgtttg | cgaccatgtc | 1380 |
| aaagctcaaa | gagcagctaa | ccaagggtcaa | agaatgttac | tccccactcc | tttatgagtc | 1440 |
| tcagcagctg | ttgattccgt | tggaggaatt | agaaaagcag | atgacgtcct | tttatgactc | 1500 |
| acttgggaaa | atcaatgaaa | ttatcacagt | tcttgagcgt | gaggcacaat | cgagtgcctt | 1560 |
| ttttaaacaa | aaacatcagg | aactgttagc | ttgtcaagaa | aactgtaaga | aaaccttgac | 1620 |
| acttattgag | aaaggcagtc | aaagtgttca | aaagtttgtg | accttgagca | acgtgttaaa | 1680 |
| gcattttgat | cagacgaggc | tacaaagaca | gattgcagat | attcatgttg | cttttcagag | 1740 |
| tatggtaaag | aaaactggag | attggaagaa | gcatgtggaa | accaacagtc | gcttgatgaa | 1800 |
| gaagtgtgag | gagtctcgag | cagagtgtga | gaaggtagct | cggattgctc | aggagggcct | 1860 |
| ggaggaaaag | ggggatccag | aggagctcct | gcggagacac | actgagtttt | tcagtcagct | 1920 |
| ggatcagagg | gtgctcaatg | ctttcctgaa | agcttgtgat | gaactcaccg | acatccttcc | 1980 |
| agagcaggag | cagcaggggc | tgcaggaagc | tgttcgaaag | ctccacaaac | aatggaagga | 2040 |
| tcttcaagga | gaagcccctt | atcatttgct | tcattctgaag | attgatgtgg | agaagaatag | 2100 |
| gttcttagcc | tctgcagaag | aatgcagaac | tgagctggat | cgagagacca | agctgatgcc | 2160 |
| ccaggaaggc | agtgaaaaga | taattaaaga | gcacaggggt | ttcttcagtg | acaaagggtcc | 2220 |
| tcattcatct | tgtgagaaaa | ggttacagct | catcgaggaa | ctctgtgtga | aactcccagt | 2280 |
| gcgggaccca | gtaaggggaca | cacctggaac | ctgtcacgtg | actctcaaag | agctcagagc | 2340 |
| tgccattgac | agcacctaca | ggaagctcat | ggaagaccca | gacaagtgga | aggactacac | 2400 |
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 <212> DNA
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K3176SEQ.TXT

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| cctaaggagg gcgaaggaga gacagacggc gctggagaat ctgctggccc actggcagag | 1740 |
| gctagagaaa gaactatcat ccttttttgac ctgggttagag cggggtgaag ctaaagccag | 1800 |
| ttccccagaa atggacattt ctgcagacag agtcaaagtg gaaggatgaac ttcagttaat | 1860 |
| acaggcactg caaaatgaag ttgtatccca ggcctcattc tatagcaaac ttttgcaatt | 1920 |
| gaaggaatca ttgttctcag tagcctccaa agatgatgtg aaaatgatga aactacattt | 1980 |
| ggagcagttg gatgagagat ggagagattt accacagatc attaacaaaa ggattaattt | 2040 |
| tcttcagtct gtggttgctg aacaccagca atttgatgag ctgctgcttt ccttttctgt | 2100 |
| ctggattaaa ctgtttctta gtgaattaca aactacctct gagattagca taatggacca | 2160 |
| tcaagtagcc cttactcggc ataaggacca cgcagcagaa gtagagagca aaaagggcga | 2220 |
| attgcagagt ctgcagggtc acttagcaaa gttgggttct ctgggccgtg ctgaggacct | 2280 |
| ccacctctg cagggaaagg ctgaggactg cttccagctg tttgaggagg ccagccgggt | 2340 |
| tgtggagagg cggcagcttg ccctgtccca tttggcagaa ttcctccaga gccatgcctc | 2400 |
| tctgtccggc attctccgcc agctgaggca aacagtggaa gcaaccaaca gtatgaataa | 2460 |
| gaacgagtct gatttgatag aaaaggacct caatgatgct cttcaaaatg ctaaagcatt | 2520 |
| agaatctgct gccgtcagtc tggatggggc c | 2551 |

<210> 17
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| cagaaatgga catttctgca gacagagtca aagtggaagg tgaacttcag ttaatacagg | 180 |
| cactgcaaaa tgaagttgta tcccaggcct cattctatag caaacttttg caattgaagg | 240 |
| aatcattgtt ctgagtagcc tccaaagatg atgtgaaaat gatgaaacta catttgagac | 300 |
| agttggatga gagatggaga gatttaccac agatcattaa caaaaggatt aattttcttc | 360 |
| agtctgtggt tgctgaacac cagcaatttg atgagctgct gctttccttt tctgtctgga | 420 |
| ttaaactgtt tctcagtga ttacaaacta cctctgagat tagcataatg gaccatcaag | 480 |
| tagcccttac tcggcataag gaccacgcag cagaagtaga gagcaaaaag ggccaattgc | 540 |
| agagtctgca gggtcactta gcaaagttgg gttctctggg ccgtgctgag gacctccacc | 600 |
| tcctgcaggg aaaggctgag gactgcttcc agctgtttga ggaggccagc caggttggtg | 660 |
| agaggcggca gcttgccctg tcccatttgg cagaattcct ccagagccat gcctctctgt | 720 |

K3176SEQ.TXT

| | | | | | | |
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| agtctgattt | gatagaaaag | gacctcaatg | atgctcttca | aaatgctaaa | gcattagaat | 840 |
| ctgctgccgt | cagtctggat | ggtattcttt | ccaaagccca | ataccatctg | aaaatcggga | 900 |
| gctctgagca | aaggacttcc | tgagagcca | cggctgatca | gctctgtgga | gaggtagaga | 960 |
| ggatccagaa | ccttctggga | accaagcaga | gtgaggcaga | tgctctggca | gtgttgaaaa | 1020 |
| aagcattcca | agaccagaaa | gaggagcttc | tgaaaagcat | tgaggacatt | gaagaaagga | 1080 |
| ctgacaaaaga | gcgattgaaa | gaacctaccc | gccaagctct | | | 1120 |

<210> 18
 <211> 1601
 <212> DNA
 <213> Homo Sapiens

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| cagagccacg | gctgatcagc tctgtggaga ggtagagagg atccagaacc ttctgggaac 120 |
| caagcagagt | gaggcagatg ctctggcagt gttgaaaaaa gcattccaag accagaaaga 180 |
| ggagcttctg | aaaagcattg aggacattga agaaaggact gacaaagagc gattgaaaga 240 |
| acctaccgcg | caagctcttc agcagagggt aagagtgttt aatcagctag aagatgaatt 300 |
| gaattctcac | gagcatgaac tatgttgggt gaaagacaaa gccaagcaaa ttgccagaa 360 |
| agatgtagct | tttgacactg aagttgacag ggagataaac cgcttagagg tcacctggga 420 |
| tgataccaaa | agactaattc atgaaaatca gggtcagtgc tgtggactta ttgacttaat 480 |
| gagagaatat | cagaacctga aatcagctgt atctaaagtc ttagaaaatg ccagcagtgt 540 |
| gattgtaacc | agaactacca taaaagatca ggaggatctt aaatgggctt tttccaagca 600 |
| tgaaactgcc | aagaacaaaa tgaattacaa acagaaagac ttggataact ttaccagcaa 660 |
| aggaaaacac | ttgttatctg agctgaagaa aattcacagt agtgatttca gcttggtgaa 720 |
| aacagacatg | gagagcaccg tggacaaatg gctggatgta tcagagaaac ttgaagaaaa 780 |
| catggatagg | ctgagagtaa gcctgtccat ttggggtgat gtactgtcaa ctagagatga 840 |
| gattgagggg | tggtcaaaca actgcgttcc acagatggca gaaaacatca gcaacctgga 900 |
| taaccacctc | agagctgaag aactgcctaa agaatttgag tctgaagtta aaaacaaagc 960 |
| attgagattg | gaagaactgc attccaaagt taatgatctg aaagaattaa ctaaaaatct 1020 |
| agaaacaccg | ccagaccttc agtttataga agcagactta atgcagaaac tggagcatgc 1080 |
| caaagaaata | actgaagtag caaaaggaac cctgaaggat ttcacggctc aaagtacaca 1140 |
| agtggagaag | tttattaatg acataacaac atgggttcaca aaagtgggaag aatcgttgat 1200 |
| gaactgtgcc | caaaatgaga cttgtgaagc attgaaaaaa gtcaaggata tacaaaaaga 1260 |

K3176SEQ.TXT

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| acttcaaagt | caacaaagca | acatcagctc | tacccaagaa | aatctcaata | gcttgtgccg | 1320 |
| caagtaccac | tcagctgagt | tggagagcct | gggccgtgca | atgactggtc | tgataaagaa | 1380 |
| acatgaagcc | gtgagccagt | tgtgctccaa | aaccaggcc | agcctgcagg | aatctctgga | 1440 |
| aaaacacttc | agtgagtcta | tgagggaatt | ccaagaatgg | tttttgggag | caaaggcagc | 1500 |
| agcaaaagaa | tcatcagatc | gcaccggtga | cagcaaagtt | ctagaagcaa | agctccatga | 1560 |
| tcttcagaac | attttggact | cagtcagtga | tgggcagagc | a | | 1601 |

<210> 19

<211> 1694

<212> DNA

<213> Homo sapiens

<400> 19

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| cccaggccag | cctgcaggaa | tctctggaaa | aacacttcag | tgagtctatg | caggaattcc | 120 |
| agaatgggt | tttgggagca | aaggcagcag | caaaagaatc | atcagatcgc | accggtgaca | 180 |
| gcaaagttct | agaagcaaag | ctccatgatc | ttcagaacat | tttggactca | gtcagtgatg | 240 |
| ggcagagcaa | acttgatgca | gtgactcaag | aaggacaaaac | tttgtatgca | catttgtcta | 300 |
| aacaaattgt | cagtagcatt | caagaacaaa | tcacaaaggc | caatgaagag | tttcaagcat | 360 |
| ttctgaaaca | atgccttaaa | gataagcagg | ctcttcaaga | ctgtgcttca | gaacttggaa | 420 |
| gctttgaaga | tcagcacaga | aaactgaact | tatggatcca | tgaaatggaa | gaaaggttca | 480 |
| atacgaaaa | cttgggagag | agtaaacagc | acattcctga | gaagaaaaat | gaagttcata | 540 |
| aagttgaaat | gtttttggga | gaactgctgg | ctgcaagaga | gtctcttgat | aagctttccc | 600 |
| agagagggga | gcttctgagt | gaagaaggcc | acggtgctgg | gcaggagggc | cgctgtgtt | 660 |
| cccagctcct | cacaagccac | cagaacctac | ttagaatgac | caaagagaaa | ctccggagct | 720 |
| gccaggtggc | ccttcaggag | cacgaagccc | tggaggaagc | actgcaaagc | atgtggttct | 780 |
| gggtgaaggc | cattcaggac | agactggcct | gtgcagagag | cactcttggg | agcaaagaca | 840 |
| ccctggagaa | acggctgtca | caaatacagg | atattctcct | gatgaaaggt | gaaggggaag | 900 |
| ttaagttgaa | tatggccatt | ggcaaggggg | aacaggcctt | gagaagtagc | aacaaagaag | 960 |
| gtcagagggg | gattcagact | cagttagaga | cccttaaaga | agtgtgggct | gacatcatga | 1020 |
| gctcctccgt | ccacgctcaa | agcactttag | agtctgtgat | tagccaatgg | aatgactatg | 1080 |
| tagagaggaa | aaaccagttg | gagcagtgga | tggaatcagt | ggatcaaaaa | atagaacatc | 1140 |
| cctcacaaac | acagccaggt | ctgaaagaga | agttcgtcct | gcttgaccac | ctccagtcca | 1200 |
| tcctgtctga | ggcagaagat | cacacgagag | cccttcaccg | tctaattgcg | aagtccaggg | 1260 |
| agttctacga | aaagacagag | gatgagtctt | tcaaggacac | agctcaagag | gagctgaaaa | 1320 |

K3176SEQ.TXT

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|------|
| cacagtttaa | tgatataatg | actgttgcca | aggaaaaaat | gaggaaagt | gaagagattg | 1380 |
| tgaaagatca | tctaattgtat | ttagatgcgg | tccacgagtt | cacagattgg | ctccattcag | 1440 |
| caaaggaaga | acttcaccgg | tggtcagata | tgtctggaga | ttcatcagcc | accagaaaa | 1500 |
| agttatcaaa | aattaaggag | ctgatagatt | ccagagagat | tggtgcaagc | cgtctcagca | 1560 |
| gagtggagtc | gctggctccc | gaagtgaaac | agaacacaac | tgccagtggg | tgtgagctca | 1620 |
| tgcacacgga | gatgcaggcc | ctgcgtgccg | actggaagca | gtgggaagac | agtgtattcc | 1680 |
| aaacgcagag | ctgt | | | | | 1694 |

<210> 20
 <211> 1505
 <212> DNA
 <213> Homo sapiens

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| ctgccaggtg | gcccttcagg | agcacgaagc | cctggaggaa | gactgcaaa | gcatgtggtt | 120 |
| ctgggtgaag | gccattcagg | acagactggc | ctgtgcagag | agcactcttg | ggagcaaaga | 180 |
| caccctggag | aaacggctgt | cacaaataca | ggatattctc | ctgatgaaag | gtggagggga | 240 |
| agttaagttg | aatatggcca | ttggcaaggg | ggaacaggcc | ttgagaagta | gcaacaaaga | 300 |
| aggtcagagg | gtgattcaga | ctcagttaga | gacccttaaa | gaagtgtggg | ctgacatcat | 360 |
| gagctcctcc | gtccacgctc | aaagcacttt | agagtctgtg | attagccaat | ggaatgacta | 420 |
| tgtagagagg | aaaaaccagt | tggagcagtg | gatggaatca | gtggatcaaa | aaatagaaca | 480 |
| tcccttacia | ccacagccag | gtctgaaaga | gaagttcgtc | ctgcttgacc | acctccagtc | 540 |
| catcctgtct | gaggcagaag | atcacacgag | agcccttcac | cgtctaattg | tgaagtccag | 600 |
| ggagctctac | gaaaagacag | aggatgagtc | tttcaaggac | acagctcaag | aggagctgaa | 660 |
| aacacagttt | aatgatataa | tgactgttgc | caaggaaaaa | atgaggaaa | tggaagagat | 720 |
| tgtgaaagat | catctaattg | atttagatgc | ggtccacgag | ttcacagatt | ggctccattc | 780 |
| agcaaaggaa | gaacttcacc | ggtggtcaga | tatgtctgga | gattcatcag | ccaccagaa | 840 |
| aaagtatatca | aaaattaagg | agctgataga | ttccagagag | attggtgcaa | gccgtctcag | 900 |
| cagagtggag | tcgctggctc | ccgaagtga | acagaacaca | actgccagt | ggtgtgagct | 960 |
| catgcacacg | gagatgcagg | ccctgcgtgc | cgactggaag | cagtgggaag | acagtgtatt | 1020 |
| ccaaacgcag | agctgttttg | agaacctgg | cagccagatg | gccctttcgg | agcaggaatt | 1080 |
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| ctgggctcag | cagttaacct | tcctggaagg | caagaacacg | gatgaggaga | tagtggaatg | 1200 |
| ctggcacaaa | ggacaagaga | tactggatgc | tttgcaaaaa | gcagagccta | gaacagagga | 1260 |

K3176SEQ.TXT

| | | | | | | |
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| tctcaagtct | cagctgaatg | aactttgtcg | attttccaga | gacctgagta | cctacagtgg | 1320 |
| aaaagtttct | ggcttgatta | aagagtataa | ttggtgagca | tgaaccttat | tggtgttcaa | 1380 |
| gatattttta | tacaaattag | aagctagaag | tttattttta | ggtgtaattt | caaaataata | 1440 |
| ttagttcagc | attaaatata | ttactaagtg | aggtaagtgc | acattctaag | aactggtgac | 1500 |
| ccggg | | | | | | 1505 |

<210> 21
 <211> 681
 <212> DNA
 <213> Homo sapiens

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| cttcaggagc | acgaagccct | ggaggaagca | ctgcaaagca | tgtggttctg | ggtgaaggcc | 120 |
| attcaggaca | gactggcctg | tgcagagagc | actcttgggg | gcaaagacac | cctggagaaa | 180 |
| cggctgtcac | aaatacagga | tattctcctg | atgaaaggtg | aaggggaagt | taagttgaat | 240 |
| atggccattg | gcaaggggga | acaggccttg | agaagtagca | acaagaagg | tcagaggggtg | 300 |
| attcagactc | agttagagac | ccttaaagaa | gtgtgggctg | acatcatgag | ctcctccgtc | 360 |
| cacgctcaaa | gcactttaga | gtctgtgatt | agccaatgga | atgactatgt | agagaggaaa | 420 |
| aaccagttgg | agcagtggat | ggaatcagtg | gatcaaaaaa | tagaacatcc | cttacaacca | 480 |
| cagccaggtc | tgaaagagaa | gttcgtcctg | cttgaccacc | tccagtccat | cctgtctgag | 540 |
| gcagaagatc | acacgagagc | ccttcaccgt | ctaattgcga | agtccaggga | gctctacgaa | 600 |
| aagacagagg | atgagtcttt | caaggacaca | gctcaagagg | agctgaaaac | acagtttaat | 660 |
| gatataatga | ctgttgccaa | a | | | | 681 |

<210> 22
 <211> 24
 <212> DNA
 <213> Homo sapiens

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|------------|------------|------|--|--|--|----|
| <400> 22 | | | | | | |
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<210> 23
 <211> 28
 <212> DNA
 <213> Homo sapiens

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|------------|------------|----------|--|--|--|----|
| <400> 23 | | | | | | |
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<210> 24
 <211> 1093
 <212> DNA

K3176SEQ.TXT

<213> Homo sapiens

<400> 24

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| aaggagctga tagattccag agagattggt gcaagccgtc tcagcagagt ggagtcgctg | 180 |
| gctcccgaag tgaaacagaa cacaactgcc agtgggtgtg agctcatgca cacggagatg | 240 |
| caggccctgc gtgccgactg gaagcagtgg gaagacagtg tattccaaac gcagagctgt | 300 |
| ttggagaacc tggtcagcca gatggccctt tcggagcagg aattctcagg ccaagtggct | 360 |
| caactggagc aggccctgga acagttcagt gcccttctga aaacctgggc tcagcagtta | 420 |
| accctcctgg aaggcaagaa cacggatgag gagatagtgg aatgctggca caaaggacaa | 480 |
| gagatactgg atgctttgca aaaagcagag cctagaacag aggatctcaa gtctcagctg | 540 |
| aatgaacttt gtcgattttc cagagacctg agtacctaca gtggaaaagt ttctggcttg | 600 |
| attaaagagt ataattggtg agcatgaacc ttattggtgt tcaagatatt ttatacaaa | 660 |
| ttagaagcta gaagtttatt ttaaggtgta atttcaaaat aatattagtt cagcattaaa | 720 |
| tatattacta agtgaggtaa gtgcacattc taagaactgg tgattctatc aaacatgatt | 780 |
| ttcatcaact ttatcgcttt ttcttgccat taaatttttg cgtcaccttt tcagtctttg | 840 |
| tttgcaagca tccaagggct gccagaataa agaacagatt ttacagcaaa gatttcgaaa | 900 |
| ggccttcagg gatttcagc agtggttgggt taatgcaaaa atcactaccg ccaagtgttt | 960 |
| tgatatacct caaaatataa gtgaagtttc aactagtctt cagaaaatac aggtaagggt | 1020 |
| gttatcaatt aattctagta gcagtgtga tgtgaactaa agttaacctc taaatcaagg | 1080 |
| gtccccagtc gac | 1093 |

<210> 25

<211> 357

<212> DNA

<213> Homo sapiens

<400> 25

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| cccgaagtga aacagaacac aactgccagt ggggtgtgagc tcatgcacac ggagatgcag | 120 |
| gccctgctg ccgactggaa gcagtgggaa gacagtgtat tccaaacgca gagctgtttg | 180 |
| gagaacctgg tcagccagat ggccctttcg gagcaggaat tctcaggcca agtggctcaa | 240 |
| ctggagcagg ccctggaaca gttcagtgcc cttctgaaaa cctgggctca gcagttaacc | 300 |
| ctcctggaag gcaagaacac ggatgaggag atagtggaaat gctggcacia aggacaa | 357 |

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<211> 137

K3176SEQ.TXT

<212> DNA
 <213> Homo sapiens

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 attaaagagt ataattg 137

<210> 27
 <211> 878
 <212> DNA
 <213> Homo sapiens

<400> 27
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 gagtacctac agtggaaaag tttctggctt gattaaagag tataattggg gagcatgaac 180
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 aatttcaaaa taatattagt tcagcattaa atatattact aagtgaggta agtgcacatt 300
 ctaagaactg gtgattctat caaacatgat tttcatcaac tttatcgctt tttcctgcc 360
 ttaaattttt gcgtcacctt ttcagtcttt gtttgcaagc atccaagggc tgccagaata 420
 aagaacagat ttacagcaa agatttcgaa aggccttcag ggatttcag cagtgggttg 480
 ttaatgcaaa aatcactacc gccaaagtgt ttgatatacc tcaaaatata agtgaagttt 540
 caactagtct tcagaaaata caggttaagg tggtatcaat taattctagt agcagtgtg 600
 atgtgaacta aagttaacct ctaaatacaag ggtcccatc tcctgggccg cggactggta 660
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 gcgttactgc ctgagctcca cctcctgtca gatcagcggg agcatcagat tctcatagga 780
 gcctgaacct cattgtgaac tgtgcacaca gaggaactag gctgtgtgct ctttctaaga 840
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<210> 28
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 <212> DNA
 <213> Homo sapiens

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 attaaagagt ataattgggtg agcatgaacc ttattggtgt tcaagatatt ttatacaaaa 180
 ttagaagcta gaagtttatt ttaagggtgta atttcaaaat aatattagtt cagcattaaa 240
 tatattacta agtgaggtaa gtgcacattc taagaactgg tgattctatc aaacatgatt 300

K3176SEQ.TXT

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ttcatcaact ttatcgcttt ttcctgccat taaatttttg cgtcaccttt tcagtctttg 360
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ggccttcagg gatttcagc agtggttggg taatgcaaaa atcactaccg ccaagtgttt 480
tgatatacct caaaatataa gtgaagtttc aactagtctt cagaaaatac aggtaagggt 540
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<210> 29
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<212> DNA
<213> Homo sapiens

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<212> PRT
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<400> 30

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Val Met Gln Arg Leu Gln Asp Glu Gln Glu Ile Val Gln Lys Arg Thr
20          25          30

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Phe Thr Lys Trp Ile Asn Ser His Leu Ala Lys Arg Lys Pro Pro Met
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Val Val Asp Asp Leu Phe Glu Asp Met Lys Asp Gly Val Lys Leu Leu
50          55          60

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Ala Leu Leu Glu Val Leu Ser Gly Gln Lys Leu Pro Cys Glu Gln Gly
65          70          75          80

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Arg Arg Met Lys Arg Ile His Ala Val Ala Asn Ile Gly Thr Ala Leu
85          90          95

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Lys Phe Leu Glu Gly Arg Lys Ile Lys Leu Val Asn Ile Asn Ser Thr

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K3176SEQ.TXT

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| Asp Ile Ala Asp Gly Arg Pro Ser Ile Val Leu Gly Leu Met Trp Thr | 115 | 120 | 125 | |
| Ile Ile Leu Tyr Phe Gln Ile Glu Glu Leu Thr Ser Asn Leu Pro Gln | 130 | 135 | 140 | |
| Leu Gln Ser Leu Ser Ser Ser Ala Ser Ser Val Asp Ser Ile Val Ser | 145 | 150 | 155 | 160 |
| Ser Glu Thr Pro Ser Pro Pro Ser Lys Arg Lys Val Thr Thr Lys Ile | 165 | 170 | 175 | |
| Gln Gly Asn Ala Lys Lys Ala Leu Leu Lys Trp Val Gln Tyr Thr Ala | 180 | 185 | 190 | |
| Gly Lys Gln Thr Gly Ile Glu Val Lys Asp Phe Gly Lys Ser Trp Arg | 195 | 200 | 205 | |
| Ser Gly Val Ala Phe His Ser Val Ile His Ala Ile Arg Pro Glu Leu | 210 | 215 | 220 | |
| Val Asp Leu Glu Thr Val Lys Gly Arg Ser Asn Arg Glu Asn Leu Glu | 225 | 230 | 235 | 240 |
| Asp Ala Phe Thr Ile Ala Glu Thr Glu Leu Gly Ile Pro Arg Leu Leu | 245 | 250 | 255 | |
| Asp Pro Glu Asp Val Asp Val Asp Lys Pro Asp Glu Lys Ser Ile Met | 260 | 265 | 270 | |
| Thr Tyr Val Ala Gln Phe Leu Lys His Tyr Pro Asp Ile His Asn Ala | 275 | 280 | 285 | |
| Ser Thr Asp Gly Gln Glu Asp Asp Arg Glu Asp Arg Val Ile Phe Lys | 290 | 295 | 300 | |
| Glu Met Lys Val Trp Ile Glu Gln Phe Glu Arg Asp Leu Thr Arg Ala | 305 | 310 | 315 | 320 |
| Gln Met Val Glu Ser Asn Leu Gln Asp Lys Tyr Gln Ser Phe Lys His | 325 | 330 | 335 | |
| Phe Arg Val Gln Tyr Glu Met Lys Arg Lys Gln Ile Glu His Leu Ile | 340 | 345 | 350 | |

K3176SEQ.TXT

Gln Pro Leu His Arg Asp Gly Lys Leu Ser Leu Asp Gln Ala Leu Val
 355 360 365
 Lys Gln Ser Trp Asp Arg Val Thr Ser Arg Leu Phe Asp Trp His Ile
 370 375 380
 Gln Leu Asp Lys Ser Leu Pro Ala Pro Leu Gly Thr Ile Gly Ala Trp
 385 390 395 400
 Leu Tyr Arg Ala Glu Val Ala Leu Arg Glu Glu Ile Thr Val Gln Gln
 405 410 415
 Val His Glu Glu Thr Ala Asn Thr Ile Gln Arg Lys Leu Glu Gln His
 420 425 430
 Lys Asp Leu Leu Gln Asn Thr Asp Ala His Lys Arg Ala Phe His Glu
 435 440 445
 Ile Tyr Arg Thr Arg Ser Val Asn Gly Ile Pro Val Pro Pro Asp Gln
 450 455 460
 Leu Glu Asp Met Ala Glu Arg Phe His Phe Val Ser Ser Thr Ser Glu
 465 470 475 480
 Leu His Leu Met Lys Met Glu Phe Leu Glu Leu Lys Tyr Arg Leu Leu
 485 490 495
 Ser Leu Leu Val Leu Ala Glu Ser Lys Leu Lys Ser Trp Ile Ile Lys
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 Tyr Gly Arg Arg Glu Ser Val Glu Gln Leu Leu Gln Asn Tyr Val Ser
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 Phe Ile Glu Asn Ser Lys Phe Phe Glu Gln Tyr Glu Val Thr Tyr Gln
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 Ile Leu Lys Gln Thr Ala Glu Met Tyr Val Lys Ala Asp Gly Ser Val
 545 550 555 560
 Glu Glu Ala Glu Asn Val Met Lys Phe Met Asn Glu Thr Thr Ala Gln
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 580 585 590
 Glu Val Ile Ser Asn Trp Asp Arg Tyr Gly Asn Thr Val Ala Ser Leu
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K3176SEQ.TXT

Gln Ala Trp Leu Glu Asp Ala Glu Lys Met Leu Asn Gln Ser Glu Asn
 610 615 620
 Ala Lys Lys Asp Phe Phe Arg Asn Leu Pro His Trp Ile Gln Gln His
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 Thr Ala Met Asn Asp Ala Gly Asn Phe Leu Ile Glu Thr Cys Asp Glu
 645 650 655
 Met Val Ser Arg Asp Leu Lys Gln Gln Leu Leu Leu Leu Asn Gly Arg
 660 665 670
 Trp Arg Glu Leu Phe Met Glu Val Lys Gln Tyr Ala Gln Ala Asp Glu
 675 680 685
 Met Asp Arg Met Lys Lys Glu Tyr Thr Asp Cys Val Val Thr Leu Ser
 690 695 700
 Ala Phe Ala Thr Glu Ala His Lys Lys Leu Ser Glu Pro Leu Glu Val
 705 710 715 720
 Ser Phe Met Asn Val Lys Leu Leu Ile Gln Asp Leu Glu Asp Ile Glu
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 Gln Arg Val Pro Val Met Asp Ala Gln Tyr Lys Ile Ile Thr Lys Thr
 740 745 750
 Ala His Leu Ile Thr Lys Glu Ser Pro Gln Glu Glu Gly Lys Glu Met
 755 760 765
 Phe Ala Thr Met Ser Lys Leu Lys Glu Gln Leu Thr Lys Val Lys Glu
 770 775 780
 Cys Tyr Ser Pro Leu Leu Tyr Glu Ser Gln Gln Leu Leu Ile Pro Leu
 785 790 795 800
 Glu Glu Leu Glu Lys Gln Met Thr Ser Phe Tyr Asp Ser Leu Gly Lys
 805 810 815
 Ile Asn Glu Ile Ile Thr Val Leu Glu Arg Glu Ala Gln Ser Ser Ala
 820 825 830
 Leu Phe Lys Gln Lys His Gln Glu Leu Leu Ala Cys Gln Glu Asn Cys
 835 840 845
 Lys Lys Thr Leu Thr Leu Ile Glu Lys Gly Ser Gln Ser Val Gln Lys
 850 855 860

K3176SEQ.TXT

Phe Val Thr Leu Ser Asn Val Leu Lys His Phe Asp Gln Thr Arg Leu
865 870 875 880

Gln Arg Gln Ile Ala Asp Ile His Val Ala Phe Gln Ser Met Val Lys
885 890 895

Lys Thr Gly Asp Trp Lys Lys His Val Glu Thr Asn Ser Arg Leu Met
900 905 910

Lys Lys Phe Glu Glu Ser Arg Ala Glu Leu Glu Lys Val Leu Arg Ile
915 920 925

Ala Gln Glu Gly Leu Glu Glu Lys Gly Asp Pro Glu Glu Leu Leu Arg
930 935 940

Arg His Thr Glu Phe Phe Ser Gln Leu Asp Gln Arg Val Leu Asn Ala
945 950 955 960

Phe Leu Lys Ala Cys Asp Glu Leu Thr Asp Ile Leu Pro Glu Gln Glu
965 970 975

Gln Gln Gly Leu Gln Glu Ala Val Arg Lys Leu His Lys Gln Trp Lys
980 985 990

Asp Leu Gln Gly Glu Ala Pro Tyr His Leu Leu His Leu Lys Ile Asp
995 1000 1005

Val Glu Lys Asn Arg Phe Leu Ala Ser Val Glu Glu Cys Arg Thr
1010 1015 1020

Glu Leu Asp Arg Glu Thr Lys Leu Met Pro Gln Glu Gly Ser Glu
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Lys Ile Ile Lys Glu His Arg Val Phe Phe Ser Asp Lys Gly Pro
1040 1045 1050

His His Leu Cys Glu Lys Arg Leu Gln Leu Ile Glu Glu Leu Cys
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Val Lys Leu Pro Val Arg Asp Pro Val Arg Asp Thr Pro Gly Thr
1070 1075 1080

Cys His Val Thr Leu Lys Glu Leu Arg Ala Ala Ile Asp Ser Thr
1085 1090 1095

Tyr Arg Lys Leu Met Glu Asp Pro Asp Lys Trp Lys Asp Tyr Thr
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K3176SEQ.TXT

Leu Phe Gln Thr Gly Ser Ser His Glu Arg Phe Leu Ser Phe Ser
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 1370 1375 1380
 Lys Glu Ala Ser Glu Ile Pro Leu Gly Pro Gln Asn Lys Gln Leu
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 1400 1405 1410
 Glu Asp Thr Leu Glu Glu Asp Ile Lys Thr Met Glu Met Val Lys
 1415 1420 1425
 Thr Lys Trp Asp His Phe Gly Ser Asn Phe Glu Thr Leu Ser Val
 1430 1435 1440
 Trp Ile Thr Glu Lys Glu Lys Glu Leu Asn Ala Leu Glu Thr Ser
 1445 1450 1455
 Ser Ser Ala Met Asp Met Gln Ile Ser Gln Ile Lys Val Thr Ile
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 Gln Glu Ile Glu Ser Lys Leu Ser Ser Ile Val Gly Leu Glu Glu
 1475 1480 1485
 Glu Ala Gln Ser Phe Ala Gln Phe Val Thr Thr Gly Glu Ser Ala
 1490 1495 1500
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K3176SEQ.TXT

Met Asp Leu Cys Gln Ala Leu Glu Ser Leu Ser Ser Ala Ile Thr
 1580 1585 1590
 Ala Phe Ser Ala Ser Ala Arg Lys Val Val Asn Arg Asp Ser Cys
 1595 1600 1605
 Val Gln Glu Ala Ala Ala Leu Gln Gln Gln Tyr Glu Asp Ile Leu
 1610 1615 1620
 Arg Arg Ala Lys Glu Arg Gln Thr Ala Leu Glu Asn Leu Leu Ala
 1625 1630 1635
 His Trp Gln Arg Leu Glu Lys Glu Leu Ser Ser Phe Leu Thr Trp
 1640 1645 1650
 Leu Glu Arg Gly Glu Ala Lys Ala Ser Ser Pro Glu Met Asp Ile
 1655 1660 1665
 Ser Ala Asp Arg Val Lys Val Glu Gly Glu Leu Gln Leu Ile Gln
 1670 1675 1680
 Ala Leu Gln Asn Glu Val Val Ser Gln Ala Ser Phe Tyr Ser Lys
 1685 1690 1695
 Leu Leu Gln Leu Lys Glu Ser Leu Phe Ser Val Ala Ser Lys Asp
 1700 1705 1710
 Asp Val Lys Met Met Lys Leu His Leu Glu Gln Leu Asp Glu Arg
 1715 1720 1725
 Trp Arg Asp Leu Pro Gln Ile Ile Asn Lys Arg Ile Asn Phe Leu
 1730 1735 1740
 Gln Ser Val Val Ala Glu His Gln Gln Phe Asp Glu Leu Leu Leu
 1745 1750 1755
 Ser Phe Ser Val Trp Ile Lys Leu Phe Leu Ser Glu Leu Gln Thr
 1760 1765 1770
 Thr Ser Glu Ile Ser Ile Met Asp His Gln Val Ala Leu Thr Arg
 1775 1780 1785
 His Lys Asp His Ala Ala Glu Val Glu Ser Lys Lys Gly Glu Leu
 1790 1795 1800
 Gln Ser Leu Gln Gly His Leu Ala Lys Leu Gly Ser Leu Gly Arg
 1805 1810 1815

K3176SEQ.TXT

Ala Glu Asp Leu His Leu Leu Gln Gly Lys Ala Glu Asp Cys Phe
 1820 1825 1830
 Gln Leu Phe Glu Glu Ala Ser Gln Val Val Glu Arg Arg Gln Leu
 1835 1840 1845
 Ala Leu Ser His Leu Ala Glu Phe Leu Gln Ser His Ala Ser Leu
 1850 1855 1860
 Ser Gly Ile Leu Arg Gln Leu Arg Gln Thr Val Glu Ala Thr Asn
 1865 1870 1875
 Ser Met Asn Lys Asn Glu Ser Asp Leu Ile Glu Lys Asp Leu Asn
 1880 1885 1890
 Asp Ala Leu Gln Asn Ala Lys Ala Leu Glu Ser Ala Ala Val Ser
 1895 1900 1905
 Leu Asp Gly Ile Leu Ser Lys Ala Gln Tyr His Leu Lys Ile Gly
 1910 1915 1920
 Ser Ser Glu Gln Arg Thr Ser Cys Arg Ala Thr Ala Asp Gln Leu
 1925 1930 1935
 Cys Gly Glu Val Glu Arg Ile Gln Asn Leu Leu Gly Thr Lys Gln
 1940 1945 1950
 Ser Glu Ala Asp Ala Leu Ala Val Leu Lys Lys Ala Phe Gln Asp
 1955 1960 1965
 Gln Lys Glu Glu Leu Leu Lys Ser Ile Glu Asp Ile Glu Glu Arg
 1970 1975 1980
 Thr Asp Lys Glu Arg Leu Lys Glu Pro Thr Arg Gln Ala Leu Gln
 1985 1990 1995
 Gln Arg Leu Arg Val Phe Asn Gln Leu Glu Asp Glu Leu Asn Ser
 2000 2005 2010
 His Glu His Glu Leu Cys Trp Leu Lys Asp Lys Ala Lys Gln Ile
 2015 2020 2025
 Ala Gln Lys Asp Val Ala Phe Ala Pro Glu Val Asp Arg Glu Ile
 2030 2035 2040
 Asn Arg Leu Glu Val Thr Trp Asp Asp Thr Lys Arg Leu Ile His

K3176SEQ.TXT
2055

| | | | | | | | | | | | | | | |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| 2045 | | | | | | 2050 | | | | | | | | |
| Glu | Asn | Gln | Gly | Gln | Cys | Cys | Gly | Leu | Ile | Asp | Leu | Met | Arg | Glu |
| 2060 | | | | | | 2065 | | | | | 2070 | | | |
| Tyr | Gln | Asn | Leu | Lys | Ser | Ala | Val | Ser | Lys | Val | Leu | Glu | Asn | Ala |
| 2075 | | | | | | 2080 | | | | | 2085 | | | |
| Ser | Ser | Val | Ile | Val | Thr | Arg | Thr | Thr | Ile | Lys | Asp | Gln | Glu | Asp |
| 2090 | | | | | | 2095 | | | | | 2100 | | | |
| Leu | Lys | Trp | Ala | Phe | Ser | Lys | His | Glu | Thr | Ala | Lys | Asn | Lys | Met |
| 2105 | | | | | | 2110 | | | | | 2115 | | | |
| Asn | Tyr | Lys | Gln | Lys | Asp | Leu | Asp | Asn | Phe | Thr | Ser | Lys | Gly | Lys |
| 2120 | | | | | | 2125 | | | | | 2130 | | | |
| His | Leu | Leu | Ser | Glu | Leu | Lys | Lys | Ile | His | Ser | Ser | Asp | Phe | Ser |
| 2135 | | | | | | 2140 | | | | | 2145 | | | |
| Leu | Val | Lys | Thr | Asp | Met | Glu | Ser | Thr | Val | Asp | Lys | Trp | Leu | Asp |
| 2150 | | | | | | 2155 | | | | | 2160 | | | |
| Val | Ser | Glu | Lys | Leu | Glu | Glu | Asn | Met | Asp | Arg | Leu | Arg | Val | Ser |
| 2165 | | | | | | 2170 | | | | | 2175 | | | |
| Leu | Ser | Ile | Trp | Asp | Asp | Val | Leu | Ser | Thr | Arg | Asp | Glu | Ile | Glu |
| 2180 | | | | | | 2185 | | | | | 2190 | | | |
| Gly | Trp | Ser | Asn | Asn | Cys | Val | Pro | Gln | Met | Ala | Glu | Asn | Ile | Ser |
| 2195 | | | | | | 2200 | | | | | 2205 | | | |
| Asn | Leu | Asp | Asn | His | Leu | Arg | Ala | Glu | Glu | Leu | Leu | Lys | Glu | Phe |
| 2210 | | | | | | 2215 | | | | | 2220 | | | |
| Glu | Ser | Glu | Val | Lys | Asn | Lys | Ala | Leu | Arg | Leu | Glu | Glu | Leu | His |
| 2225 | | | | | | 2230 | | | | | 2235 | | | |
| Ser | Lys | Val | Asn | Asp | Leu | Lys | Glu | Leu | Thr | Lys | Asn | Leu | Glu | Thr |
| 2240 | | | | | | 2245 | | | | | 2250 | | | |
| Pro | Pro | Asp | Leu | Gln | Phe | Ile | Glu | Ala | Asp | Leu | Met | Gln | Lys | Leu |
| 2255 | | | | | | 2260 | | | | | 2265 | | | |
| Glu | His | Ala | Lys | Glu | Ile | Thr | Glu | Val | Ala | Lys | Gly | Thr | Leu | Lys |
| 2270 | | | | | | 2275 | | | | | 2280 | | | |

K3176SEQ.TXT

Asp Phe Thr Ala Gln Ser Thr Gln Val Glu Lys Phe Ile Asn Asp
 2285 2290 2295
 Ile Thr Thr Trp Phe Thr Lys Val Glu Glu Ser Leu Met Asn Cys
 2300 2305 2310
 Ala Gln Asn Glu Thr Cys Glu Ala Leu Lys Lys Val Lys Asp Ile
 2315 2320 2325
 Gln Lys Glu Leu Gln Ser Gln Gln Ser Asn Ile Ser Ser Thr Gln
 2330 2335 2340
 Glu Asn Leu Asn Ser Leu Cys Arg Lys Tyr His Ser Ala Glu Leu
 2345 2350 2355
 Glu Ser Leu Gly Arg Ala Met Thr Gly Leu Ile Lys Lys His Glu
 2360 2365 2370
 Ala Val Ser Gln Leu Cys Ser Lys Thr Gln Ala Ser Leu Gln Glu
 2375 2380 2385
 Ser Leu Glu Lys His Phe Ser Glu Ser Met Gln Glu Phe Gln Glu
 2390 2395 2400
 Trp Phe Leu Gly Ala Lys Ala Ala Ala Lys Glu Ser Ser Asp Arg
 2405 2410 2415
 Thr Gly Asp Ser Lys Val Leu Glu Ala Lys Leu His Asp Leu Gln
 2420 2425 2430
 Asn Ile Leu Asp Ser Val Ser Asp Gly Gln Ser Lys Leu Asp Ala
 2435 2440 2445
 Val Thr Gln Glu Gly Gln Thr Leu Tyr Ala His Leu Ser Lys Gln
 2450 2455 2460
 Ile Val Ser Ser Ile Gln Glu Gln Ile Thr Lys Ala Asn Glu Glu
 2465 2470 2475
 Phe Gln Ala Phe Leu Lys Gln Cys Leu Lys Asp Lys Gln Ala Leu
 2480 2485 2490
 Gln Asp Cys Ala Ser Glu Leu Gly Ser Phe Glu Asp Gln His Arg
 2495 2500 2505
 Lys Leu Asn Leu Trp Ile His Glu Met Glu Glu Arg Phe Asn Thr
 2510 2515 2520

K3176SEQ.TXT

Glu Asn Leu Gly Glu Ser Lys Gln His Ile Pro Glu Lys Lys Asn
 2525 2530 2535
 Glu Val His Lys Val Glu Met Phe Leu Gly Glu Leu Leu Ala Ala
 2540 2545 2550
 Arg Glu Ser Leu Asp Lys Leu Ser Gln Arg Gly Gln Leu Leu Ser
 2555 2560 2565
 Glu Glu Gly His Gly Ala Gly Gln Glu Gly Arg Leu Cys Ser Gln
 2570 2575 2580
 Leu Leu Thr Ser His Gln Asn Leu Leu Arg Met Thr Lys Glu Lys
 2585 2590 2595
 Leu Arg Ser Cys Gln Val Ala Leu Gln Glu His Glu Ala Leu Glu
 2600 2605 2610
 Glu Ala Leu Gln Ser Met Trp Phe Trp Val Lys Ala Ile Gln Asp
 2615 2620 2625
 Arg Leu Ala Cys Ala Glu Ser Thr Leu Gly Ser Lys Asp Thr Leu
 2630 2635 2640
 Glu Lys Arg Leu Ser Gln Ile Gln Asp Ile Leu Leu Met Lys Gly
 2645 2650 2655
 Glu Gly Glu Val Lys Leu Asn Met Ala Ile Gly Lys Gly Glu Gln
 2660 2665 2670
 Ala Leu Arg Ser Ser Asn Lys Glu Gly Gln Arg Val Ile Gln Thr
 2675 2680 2685
 Gln Leu Glu Thr Leu Lys Glu Val Trp Ala Asp Ile Met Ser Ser
 2690 2695 2700
 Ser Val His Ala Gln Ser Thr Leu Glu Ser Val Ile Ser Gln Trp
 2705 2710 2715
 Asn Asp Tyr Val Glu Arg Lys Asn Gln Leu Glu Gln Trp Met Glu
 2720 2725 2730
 Ser Val Asp Gln Lys Ile Glu His Pro Leu Gln Pro Gln Pro Gly
 2735 2740 2745
 Leu Lys Glu Lys Phe Val Leu Leu Asp His Leu Gln Ser Ile Leu
 2750 2755 2760

K3176SEQ.TXT

Ser Glu Ala Glu Asp His Thr Arg Ala Leu His Arg Leu Ile Ala
 2765 2770 2775
 Lys Ser Arg Glu Leu Tyr Glu Lys Thr Glu Asp Glu Ser Phe Lys
 2780 2785 2790
 Asp Thr Ala Gln Glu Glu Leu Lys Thr Gln Phe Asn Asp Ile Met
 2795 2800 2805
 Thr Val Ala Lys Glu Lys Met Arg Lys Val Glu Glu Ile Val Lys
 2810 2815 2820
 Asp His Leu Met Tyr Leu Asp Ala Val His Glu Phe Thr Asp Trp
 2825 2830 2835
 Leu His Ser Ala Lys Glu Glu Leu His Arg Trp Ser Asp Met Ser
 2840 2845 2850
 Gly Asp Ser Ser Ala Thr Gln Lys Lys Leu Ser Lys Ile Lys Glu
 2855 2860 2865
 Leu Ile Asp Ser Arg Glu Ile Gly Ala Ser Arg Leu Ser Arg Val
 2870 2875 2880
 Glu Ser Leu Ala Pro Glu Val Lys Gln Asn Thr Thr Ala Ser Gly
 2885 2890 2895
 Cys Glu Leu Met His Thr Glu Met Gln Ala Leu Arg Ala Asp Trp
 2900 2905 2910
 Lys Gln Trp Glu Asp Ser Val Phe Gln Thr Gln Ser Cys Leu Glu
 2915 2920 2925
 Asn Leu Val Ser Gln Met Ala Leu Ser Glu Gln Glu Phe Ser Gly
 2930 2935 2940
 Gln Val Ala Gln Leu Glu Gln Ala Leu Glu Gln Phe Ser Ala Leu
 2945 2950 2955
 Leu Lys Thr Trp Ala Gln Gln Leu Thr Leu Leu Glu Gly Lys Asn
 2960 2965 2970
 Thr Asp Glu Glu Ile Val Glu Cys Trp His Lys Gly Gln Glu Ile
 2975 2980 2985
 Leu Asp Ala Leu Gln Lys Ala Glu Pro Arg Thr Glu Asp Leu Lys
 2990 2995

K3176SEQ.TXT
3000

2990

2995

Ser Gln Leu Asn Glu Leu Cys Arg Phe Ser Arg Asp Leu Ser Thr
3005 3010 3015

Tyr Ser Gly Lys Val Ser Gly Leu Ile Lys Glu Tyr Asn Trp
3020 3025 3030